

IN THE SPECIFICATION:

On page 6, lines 1-4, please replace with the following paragraph:

C1 --In contrast to NBRE (SEQ ID NO: 3) binding by monomers, the Nur-RE binds homodimers of Nur77 and both halves of the Nur-RE are required for activity. Thus, the present invention is in contradistinction to the prior art which teaches that Nur-77 activates transcription as a monomer.--

On page 16, lines 12-16, please replace with the following paragraph:

C2 --The novel Nur response element of the present invention is a sequence which is related to the hexamer motif AGGTCA (SEQ ID NO: 3) of NBRE. Nur-RE is comprised of a half site which is an octomer sequence AAAGGTCA (SEQ ID NO: 1), in which the last 6bp constitute the core hexamer motif used to classify the nuclear receptors.--

On page 36, lines 3-10, please replace with the following paragraph:

C3 --NBRE (5'-GATCCTCGTGCGAAAAGGTCAAGCGCTA-3') (SEQ ID NO: 4) or NurRE (5'-GATCCTAGTGATATTTACCTCCAAATGCCAGGA-3') (SEQ ID NO: 5) oligonucleotides were 3'-end-labeled using Klenow polymerase and purified on polyacrylamide gels. Binding conditions and DMS interference were as previously described (Drouin et al., 1993, EMBO J. 12:145-156; Drouin et al., 1992, Mol. Endocrinol. 6:1299-1309). Typically, about 10 ng in vitro translated Nur77 synthesized with the Promega TNT SP6/T7 kit, was used in gel retardation experiments.--

On page 38, lines 22-29 and page 39, lines 1-8, please replace with the following paragraph:

C4 --The interaction of Nur77 with Nur-RE was investigated directly in binding studies using in vitro translated Nur77. Surprisingly, these binding experiments indicated that the Nur-RE binds homodimers of Nur77 in contrast to the monomeric interaction of this receptor with NBRE (Fig. 3A). The prevalence of dimeric

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conserved

complexes in gel retardation experiments suggests that dimer formation is co-operative (Fig. 3B and C). In competition experiments, both Nur-RE and NBRE exhibited similar specificity of binding (Fig. 3A). The interaction of Nur77 with Nur-RE was further defined using the DMS interference method (Fig. 3D). This analysis indicated that two Nur77 moieties interact with octamer motifs that are found in an inverse orientation and separated by 6 bp. Each motif is loosely related to the NBRE: AAAGGTCA (SEQ ID NO: 1) (Fig. 3D). The upstream octamer motif is the most conserved by comparison to NBRE. The linker scanning mutation used to localize the Nur-RE (Fig. 1A, construct 3) was targeted to this upstream motif as indicated in Figure 3D. However, this upstream motif is insufficient on its own to confer Nur-RE activity (see below).--

On page 58, lines 12-18, please replace with the following paragraph:

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--The POMC Nur-RE is constituted of an imperfect palindrome containing two motifs related to the octamer AAAGGTCA (SEQ ID NO:1) in which each half site matches this consensus motif in six of eight positions. When a perfect palindromic Nur-RE sequence was synthesized (sequence: TGA CC TTT ATT CTC AAAGG TCA) (SEQ ID NO: 33), this perfect consensus Nur-RE palindrome was found to bind Nurr1 and NOR1 with greater affinity than the Nur-RE initially identified in the POMC gene (data not shown).--